

SEQUENCE LISTING

<110> PIERRE FABRE MÉDICAMENT

<120> Use of an enterobacterium protein OmpA for specific targeting towards antigen-presenting cells

<130> D17777

<150> FR 98 14007

<151> 1998-11-06

<150> PCT/FR99/02734

<151> 1999-11-08

<160> 2

<170> PatentIn Ver. 2.2

<210> 1

<211> 1035

<212> DNA

<213> *Klebsiella pneumoniae*

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<221> exon

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Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe

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tac ggt aac ggt ttc cag aac aac aac ggt ccg acc cgt aac gat cag 144

Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln

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ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc 240
Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
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Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
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ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc 336
Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
100 105 110

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Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
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Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
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Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
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Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
165 170 175

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Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
195 200 205

gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac 672
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act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg 768
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Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
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Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
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ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt 912
Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
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act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat 960
Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
305 310 315 320

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<213> *Klebsiella pneumoniae*

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Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
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Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
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Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
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Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
100 105 110

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115 120 125

Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
130 135 140

Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
145 150 155 160

Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
165 170 175

Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
180 185 190

Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
195 200 205

Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
210 215 220

Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
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Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
245 250 255

Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
260 265 270

Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
275 280 285

Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
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Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
305 310 315 320

Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
325 330 335

Glu Val Val Thr Gln Pro Ala Gly
340